

SEQUENCE LISTING

<110> Rozzell, J. David
Bui, Peter
Hua, Ling

<120> SYNTHETIC GENES FOR ENHANCED EXPRESSION

<130> B583:40608

<150> 09/494,921

<151> 2000-01-31

<160> 79

<170> PatentIn version 3.0

<210> 1

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<213> Pseudomonas putida

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THE BIBLE


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<211> 383
<212> DNA
<213> Artificial sequence
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<212> DNA
<213> Artificial Sequence
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<400> 15
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<210> 17
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<212> DNA
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<212> DNA
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<211> 111
<212> DNA
<213> Artificial Sequence
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<210> 21
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 <212> DNA
 <213> Artificial Sequence

<400> 21
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<210> 22
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 <212> DNA
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<400> 22
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<210> 23
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 <212> DNA
 <213> Artificial Sequence

<400> 23
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<210> 25
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 <212> DNA
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<400> 25

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<210> 28
<211> 1197
<212> DNA
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<210> 31

<211> 972

<212> DNA

<213> *Sporidiobolus salmonicolor*

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<400> 32

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Q & A - Feb 00

15

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 <213> Artificial Sequence

<400> 36
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 aacggtttcg ttggttccca cggtgttgaa cagctgctgg aacacggtta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttacccc ggctatcggg ggtaccctga acgctctgcg tgctgctgct 360
 gctaccccggt cegttaaacg ttctggtctg acctcctcca ccgtttccgc tctgatcccg 420
 aaaccgaacg ttgaagggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccttgccgga atccgaccgc cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattggaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgcaaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctgggttgc 780
 ctggttctgc cacaaatcga acgtcgctgt gtttacggta ctgctggtac tttcgattgg 840
 aacaccgttc tggctacctt ccgtaaacgt taccggtcca aaaccttccc ggctgacttc 900
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
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 gaaaccgctt aa 1032

<210> 37
 <211> 343
 <212> PRT
 <213> Artificial Sequence

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
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Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu

30

Leu Val Gly Ser Glu Thr Ala
340

<210> 38
 <211> 942
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 38
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 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180
 gaagaagttg gcagggctat taaagattcc ggagtccctc gtgaggaaat ttttattact 240
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480
 acgggcaaaa ctaaagccgt tgggtgtctct aatttttcta ttaacaacat taaagaatta 540
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcatccattg 600
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg gtattgttgt tgaagcctac 660
 tcaccatttg ggagtgctaa tgctccttta ctaaaagagc aagcaattat tgatatggct 720
 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780
 gttgttctgg ccaaatcggg taatcctgaa agaattgtat ccaattttaa gattttcact 840
 ctgcctgagg atgatttcaa gactattagt aacctatcca aagtgcattg tacaaagaga 900
 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39
 <211> 313
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 39
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 Thr Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val
 20 25 30
 Asp Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr
 35 40 45
 Arg His Ile Asp Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly
 50 55 60
 Arg Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr
 65 70 75 80

Thr Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn
 85 90 95
 Lys Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met
 100 105 110
 His Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val
 115 120 125
 Leu Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys
 130 135 140
 Glu Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys
 145 150 155 160
 Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn
 165 170 175
 Ile Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr
 180 185 190
 Asn Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala
 195 200 205
 Phe Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly
 210 215 220
 Ser Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala
 225 230 235 240
 Lys Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile
 245 250 255
 Gln Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile
 260 265 270
 Val Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr
 275 280 285
 Ile Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met
 290 295 300
 Lys Trp Gly Ser Phe Pro Ile Phe Gln
 305 310

<210> 40

<211> 942

<212> DNA

<213> Artificial Sequence

<400> 40

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 atcgacgac tgaaagcagg ttaccgtcac atcgacgac cagcaatcta cctgaacgaa 180
 gaagaagtag gtcgtgcaat caaagactcc ggtgttccgc gtgaagaaat ctttatcact 240
 actaaactgt ggggtactga acagcgtgac ccggaagcag cactgaacaa atctctgaaa 300

cgtctggggtc	tggactacgt	agacctgtac	ctgatgcact	ggccgggtacc	gctgaaaact	360
gaccgtgtta	ctgatggtaa	cgttctgtgt	attccgactc	tggaagacgg	tactgtagac	420
atcgacacta	aggaatggaa	cttcatcaag	acttgggaac	tgatgcagga	actgccgaaa	480
actggtaaaa	ctaaagcagt	agggtgtttcc	aacttctcta	tcaacaacat	caaagaactg	540
ctggaatctc	cgaacaacaa	agtagtaccg	gcaactaacc	agatcgaaat	ccaccgctg	600
ctgccgcagg	acgaactgat	cgcattctgc	aaagagaaaag	gtatcgtagt	agaagcatac	660
tctccgttcg	gctctgcaaa	cgcaccgctg	ctgaaagaac	aggcaatcat	cgacatggca	720
aagaaacacg	gtgtagaacc	ggcacagctg	atcatctctt	ggtctatcca	gcgtggttac	780
gtagtactgg	caaaatctgt	aaacccgga	cgtatcgtat	ctaacttcaa	aatcttcact	840
ctgccggaag	acgacttcaa	aactatctct	aacctgtcca	aagttcacgg	tactaaacgt	900
gtagtagaca	tgaaatgggg	ttctttcccg	atcttccagt	aa		942

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<210> 41
<211> 939
<212> DNA
<213> Saccharomyces cerevisiae
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[illegible]

275

280

285

Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro Asn
290 295 300

Trp Ser Pro Phe Glu Val Phe Lys
305 310

<210> 43
<211> 942
<212> DNA
<213> Artificial Sequence

<400> 43
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atcccgc aaa tcggcctggg tacttggcaa tctaaagaaa acgacgcata caaggctggt 120
ctgactgctc tgaaggatgg ctatcgctcac attgatactg ctgctattta tcgtaacgag 180
gaccaggtag gtcaggcaat caaggactct ggcgttccgc gtgaggaaat cttcgtaact 240
accaaactgt ggtgcactca gcatcatgaa ccggaagtag cactggatca atctctgaag 300
cgtctgggtc tggactatgt tgatctgtac ctgatgcatt ggccggcgcg cctggacca 360
gcgtatatta aaaacgaaga tatcctgtct gttccgacta agaaagacgg ctctcgtgct 420
gttgacatca ctaactggaa cttcatcaag acctgggaac tgatgcagga actgccgaag 480
actggtaaaa ctaaagctgt tggcgtatct aacttctcca tcaacaacct gaaggacctg 540
ctggcatccc agggcaacaa gctgactccg gctgctaacc aagtagagat ccaccgctg 600
ctgccgcagg acgaactgat caacttctgt aaatctaaag gcattgtagt tgaagcatat 660
tctcgcgtgg gttctaccga tgcgccactg ctgaaagagc cggtaatcct ggagatcgcg 720
aagaaaaaca acgtacaacc aggtcatgta gtaatctctt ggcacgtaca gcgcggctac 780
gtagttctgc cgaagtctgt aaaccggat cgtatcaaaa ctaaccgtaa aatctttacc 840
ctgtccaccg aagatttcga agcaatcaac aacatctcca aggaaaaggg cgagaaacgt 900
gtagttcacc caaactggtc cccgtttgaa gtattcaagt aa 942

<210> 44
<211> 313
<212> PRT
<213> Artificial Sequence

<400> 44

Met Gly Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn
1 5 10 15

Thr Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys
20 25 30

Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr

35					40					45					
Arg	His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly
50					55					60					
Gln	Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr
65					70					75					80
Thr	Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp
				85					90					95	
Gln	Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met
			100					105					110		
His	Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile
		115					120					125			
Leu	Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr
130						135					140				
Asn	Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys
145					150					155					160
Thr	Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn
				165					170					175	
Leu	Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala
			180					185					190		
Asn	Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn
		195					200					205			
Phe	Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly
210					215					220					
Ser	Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala
225					230					235					240
Lys	Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val
				245					250					255	
Gln	Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile
			260					265					270		
Lys	Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala
		275					280					285			
Ile	Asn	Asn	Ile	Ser	Lys	Glu	Lys	Gly	Glu	Lys	Arg	Val	Val	His	Pro
	290					295					300				
Asn	Trp	Ser	Pro	Phe	Glu	Val	Phe	Lys							
305					310										

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<210> 45
<211> 1029
<212> DNA
<213> Saccharomyces cerevisiae
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<400> 45
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60

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 acggaggcct ttggttaaaa cccaaaattc tccatggaag ttgtcccaga catatctaag 180
 ctggacgcat ttgaccatgt tttccaaaag cacggcaagg atatcaagat agttctacat 240
 acggcctctc cattctgctt tgatatcact gacagtgaac gcgatttatt aattcctgct 300
 gtgaacggtg ttaagggaaat tctccactca attaaaaaat acgccgctga ttctgtagaa 360
 cgtgtagttc tcacctcttc ttatgcagct gtgttcgata tggcaaaaaga aaacgataag 420
 tctttaacat ttaacgaaga atcctggaac ccagctacct gggagagttg ccaaagtgc 480
 ccagttaacg cctactgtgg ttctaagaag tttgctgaaa aagcagcttg ggaatttcta 540
 gaggagaata gagactctgt aaaattcgaa ttaactgccg ttaacccagt ttacgttttt 600
 ggtccgcaaa tgtttgacaa agatgtgaaa aaacacttga acacatcttg cgaactcgtc 660
 aacagcttga tgcatttatc accagaggac aagataccgg aactatttgg tggatacatt 720
 gatgttcgtg atgttgcaaa ggctcattta gttgccttcc aaaagaggga aacaattggt 780
 caaagactaa tcgtatcgga ggccagattt actatgcagg atgttctcga tctccttaac 840
 gaagacttcc ctgttctaaa aggcaatatt ccagtgggga aaccaggttc tggtgctacc 900
 cataacaccc ttggtgctac tcttgataat aaaaagagta agaaattggt aggtttcaag 960
 ttcaggaact tgaaagagac cattgacgac actgcctccc aaattttaaa atttgagggc 1020
 agaataataa 1029

<210> 46
 <211> 342
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 46

Met Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His Ile
 1 5 10 15
 Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala Arg
 20 25 30
 Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn Pro
 35 40 45
 Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala Phe
 50 55 60
 Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu His
 65 70 75 80
 Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp Leu
 85 90 95
 Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile Lys

110

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<400> 47
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ctgctgaaag aagattacaa agttatcggg tccgcacggt ccaggaaaa agctgaaaac      120
ctgactgaag catttggtaa caaccogaag ttctctatgg aagtagtacc ggacatttct      180
aaactggacg cattcgacca cgtattocaa aagcacggta aggatatcaa gatcgactg      240
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cacactgcat ctccattctg ttttgacatc actgattctg agcgcgacct gctgattccg 300
gctgttaacg gtgttaaagg tattctgcac tctattaaga aatatgctgc tgattccgta 360
gaacgcgtag ttctgacttc ctcttatgct gcagtattcg atatggctaa agagaacgac 420
aaatccctga cttttaacga agaattcttg aacccggcta cctgggaatc ttgccagtct 480
gacccggtta acgcttattg tggctctaag aagtttgctg aaaaagctgc ttgggaattc 540
ctggaagaaa accgtgactc tgtaaagttc gagctgaccg ctgtaaaccg ggtatacgtt 600
tttggcccg c agatgttcga taaagatgta aagaagcacc tgaacacttc ctgtgaactg 660
gtaaaacttc tgatgcacct gtctccagaa gataaaatcc cggagctgtt cggcggttac 720
atcgacgttc gtgacgtagc aaaagcacat ctggtagctt tccagaagcg tgagactatc 780
ggccagcgtc tgattgtttc cgaggctcgt ttcacatgc aggatgttct ggatattctg 840
aacgaagact tcccgtact gaaaggtaac attccggtgg gtaaaccagg ctctggtgca 900
actcataaca ctctgggtgc aactctggat aacaagaagt ctaagaaact gctgggtttt 960
aaattccgta acctgaaaga aactattgac gacactgcat ctcagatcct gaaattcgaa 1020
ggtcgcatct aa 1032

<210> 48
<211> 343
<212> PRT
<213> Artificial Sequence
<400> 48

Met Gly Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His
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Ile Val Asp Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala
20 25 30
Arg Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn
35 40 45
Pro Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala
50 55 60
Phe Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu
65 70 75 80
His Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp
85 90 95
Leu Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile
100 105 110
Lys Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser
115 120 125
Tyr Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr
225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly
245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile
260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu
275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile
290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu
305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala
325

<210> 51
<211> 987
<212> DNA
<213> Artificial Sequence

<400> 51
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tatcgctgt tcgacgggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180
cgtaaagcta tctctgaagg tctggatatc cgtaaggata tctttgtagt atctaagctg 240
tggaacaact ttcatacccc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300
atgggtctgg attatctgga tctgtactat atccactttc cgatcgcat taaatacgta 360
ccgttcgaag aaaaatatcc gccgggcttt tacactggtg cagacgacga aaagaagggt 420
cacatcactg aagctcacgt accgatcatc gacattacc gtgctctgga ggaatgtgta 480
gacgaaggtc tgatcaaata tatcggtgta tctaacttcc agggttctct gatccaggat 540
ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600
accaggaac acctggttga attctgcaaa ctgcacgata tccaagtagt agcatactct 660
tctttcggtc cgcagctctt catcgaaatg gacctgcagc tggctaagac caccocgact 720
ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccggtct tactacctct 780

cagggtactgc tgcgttgggc tactcagcgt ggcacgcgtg ttatcccgaa atcttctaag 840
aaagaacgctc tgctgggtaa cctggaaatc gaaaagaaat tcactctgac cgaacaggaa 900
ctgaaagata tctctgctct gaacgctaac atccgtttca acgatccgtg gacctggctg 960
gatggtaaat tcccgaacttt cgcttaa 987

<210> 52
<211> 328
<212> PRT
<213> Artificial Sequence

<400> 52

Met Gly Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu
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Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln
20 25 30
Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys
35 40 45
Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile
50 55 60
Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu
65 70 75 80
Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys
85 90 95
Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His
100 105 110
Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro
115 120 125
Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu
130 135 140
Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val
145 150 155 160
Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser
165 170 175
Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu
180 185 190
Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe
195 200 205
Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro
210 215 220
Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr
225 230 235 240

[illegible]

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<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence
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gtagaaaaga tcatcatgcc aggtgtaacc cactggcact ctccgtactt tttcgcatat	240
ttcccgactg catcctccta cccggctatg ctggctgaca tgctgtgtgg tgctatcggc	300
tgtatcggct tttcctgggc tgcattctccg gcatgcactg agctggaaac cgttatgatg	360
gattggctgg gtaaaatgct gcagctgccg gaggcatttc tggctgggtga ggctgggtgag	420
gggtgggtgg taattcaagg ctctgcgtcc gaagctactc tgggtgtctct gctggctgct	480
cgtactaaag ttgttcgtcg tctgcaagct gcatctccgg gtctgactca ggggtgctgtt	540
ctggagaaac tggtagcgta tgcttctgat caggctcact cttccgttga gcgtgctggt	600
ctgattgggtg gtgttaagct gaaagctatt ccgtccgatg gtaagttcgc tatgcgtgca	660
tccgctctgc aagaagctct ggaacgtgac aaagctgctg gtctgattcc gttcttcgtt	720
gttgctaccc tgggtactac ctcttgctgt tctttcgaca acctgctgga agttgggtccg	780
atctgtcacg aggaggacat ctggctgcac gttgacgcag catatgctgg ctctgctttt	840
atctgtccgg aattccgtca cctgctgaac ggcgttgagt tcgctgattc tttcaacttc	900
aaccgcaca agtggctgct ggtaaacttt gattgctcgg ctatgtgggt aaaacgtcgc	960
actgatctga ccggtgcatt taaactggac ccggtatatc tgaagcattc tcaccagggt	1020
tccggcctga ttaccgatta tcgtcattgg cagctgcgcg tgggtcgtcg ttttcgttcg	1080
ctgaagatgt gggttcgtatt ccgtatgtac ggcgttaaag gtctgcaagc ataatccgt	1140
aaacacgttc aactgtcgca cgagttcgaa gctttcgtac tgcaggaccc gcgttttgaa	1200
gtttgcgctg aagttaccct gggcctgggt tgcttccgtc tgaagggttc tgatggctctg	1260
aacgaagctc tgctggagcg tattaactcg gctcgtaaaa tccacctggt tccgtgtcgt	1320
ctgcgtggtc agttcgttct gcgcttcgct atttgctcgc gtaaggtaga gtctgggtcat	1380
gttcgtctgg catgggagca catccgtggt ctggctgctg aactgctggc tgctgaagaa	1440
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<210> 56
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<400> 56

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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20							25					30			
Asp	Val	Gln	Pro	Gly	Tyr	Leu	Arg	Pro	Leu	Ile	Pro	Ala	Thr	Ala	Pro
		35					40					45			
Gln	Glu	Pro	Asp	Thr	Phe	Glu	Asp	Ile	Leu	Gln	Asp	Val	Glu	Lys	Ile
	50					55					60				
Ile	Met	Pro	Gly	Val	Thr	His	Trp	His	Ser	Pro	Tyr	Phe	Phè	Ala	Tyr
65					70					75					80
Phe	Pro	Thr	Ala	Ser	Ser	Tyr	Pro	Ala	Met	Leu	Ala	Asp	Met	Leu	Cys
				85					90					95	
Gly	Ala	Ile	Gly	Cys	Ile	Gly	Phe	Ser	Trp	Ala	Ala	Ser	Pro	Ala	Cys
			100					105					110		
Thr	Glu	Leu	Glu	Thr	Val	Met	Met	Asp	Trp	Leu	Gly	Lys	Met	Leu	Gln
		115					120					125			
Leu	Pro	Glu	Ala	Phe	Leu	Ala	Gly	Glu	Ala	Gly	Glu	Gly	Gly	Gly	Val
	130					135					140				
Ile	Gln	Gly	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Val	Ala	Leu	Leu	Ala	Ala
145					150					155					160
Arg	Thr	Lys	Val	Val	Arg	Arg	Leu	Gln	Ala	Ala	Ser	Pro	Gly	Leu	Thr
				165					170					175	
Gln	Gly	Ala	Val	Leu	Glu	Lys	Leu	Val	Ala	Tyr	Ala	Ser	Asp	Gln	Ala
			180					185					190		
His	Ser	Ser	Val	Glu	Arg	Ala	Gly	Leu	Ile	Gly	Gly	Val	Lys	Leu	Lys
		195					200					205			
Ala	Ile	Pro	Ser	Asp	Gly	Lys	Phe	Ala	Met	Arg	Ala	Ser	Ala	Leu	Gln
	210					215					220				
Glu	Ala	Leu	Glu	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Ile	Pro	Phe	Phe	Val
225					230					235					240
Val	Ala	Thr	Leu	Gly	Thr	Thr	Ser	Cys	Cys	Ser	Phe	Asp	Asn	Leu	Leu
				245					250					255	
Glu	Val	Gly	Pro	Ile	Cys	His	Glu	Glu	Asp	Ile	Trp	Leu	His	Val	Asp
			260					265					270		
Ala	Ala	Tyr	Ala	Gly	Ser	Ala	Phe	Ile	Cys	Pro	Glu	Phe	Arg	His	Leu
		275					280					285			
Leu	Asn	Gly	Val	Glu	Phe	Ala	Asp	Ser	Phe	Asn	Phe	Asn	Pro	His	Lys
	290					295				300					
Trp	Leu	Leu	Val	Asn	Phe	Asp	Cys	Ser	Ala	Met	Trp	Val	Lys	Arg	Arg
305				310						315					320
Thr	Asp	Leu	Thr	Gly	Ala	Phe	Lys	Leu	Asp	Pro	Val	Tyr	Leu	Lys	His
				325					330					335	
Ser	His	Gln	Gly	Ser	Gly	Leu	Ile	Thr	Asp	Tyr	Arg	His	Trp	Gln	Leu
			340					345					350		

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 caaacaagat acgctgaagg tactaaaaat attttgaat cattctttac cggtaaattt 1020
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<210> 58
 <211> 365
 <212> PRT
 <213> *Candida boidinii*

<400> 58

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Asp	Glu	Glu	Lys	Leu	Tyr	Gly	Cys	Thr	Glu	Asn	Lys	Leu	Gly	Ile	Ala	20	25	30	
Asn	Trp	Leu	Lys	Asp	Gln	Gly	His	Glu	Leu	Ile	Thr	Thr	Ser	Asp	Lys	35	40	45	
Glu	Gly	Glu	Thr	Ser	Glu	Leu	Asp	Lys	His	Ile	Pro	Asp	Ala	Asp	Ile	50	55	60	
Ile	Ile	Thr	Thr	Pro	Phe	His	Pro	Ala	Tyr	Ile	Thr	Lys	Glu	Arg	Leu	65	70	75	80
Asp	Lys	Ala	Lys	Asn	Leu	Lys	Leu	Val	Val	Val	Ala	Gly	Val	Gly	Ser	85	90	95	
Asp	His	Ile	Asp	Leu	Asp	Tyr	Ile	Asn	Gln	Thr	Gly	Lys	Lys	Ile	Ser	100	105	110	
Val	Leu	Glu	Val	Thr	Gly	Ser	Asn	Val	Val	Ser	Val	Ala	Glu	His	Val	115	120	125	
Val	Met	Thr	Met	Leu	Val	Leu	Val	Arg	Asn	Phe	Val	Pro	Ala	His	Glu	130	135	140	
Gln	Ile	Ile	Asn	His	Asp	Trp	Glu	Val	Ala	Ala	Ile	Ala	Lys	Asp	Ala	145	150	155	160
Tyr	Asp	Ile	Glu	Gly	Lys	Thr	Ile	Ala	Thr	Ile	Gly	Ala	Gly	Arg	Ile	165	170	175	
Gly	Tyr	Arg	Val	Leu	Glu	Arg	Leu	Leu	Pro	Phe	Asn	Pro	Lys	Glu	Leu	180	185	190	
Leu	Tyr	Tyr	Asp	Tyr	Gln	Ala	Leu	Pro	Lys	Glu	Ala	Glu	Glu	Lys	Val	195	200	205	
Gly	Ala	Arg	Arg	Val	Glu	Asn	Ile	Glu	Glu	Leu	Val	Ala	Gln	Ala	Asp	210	215	220	

225	230							235							240	
Asn	Lys	Glu	Leu	Leu	Ser	Lys	Phe	Lys	Lys	Gly	Ala	Trp	Leu	Val	Asn	
				245					250					255		
Thr	Ala	Arg	Gly	Ala	Ile	Cys	Val	Ala	Glu	Asp	Val	Ala	Ala	Ala	Leu	
			260					265					270			
Glu	Ser	Gly	Gln	Leu	Arg	Gly	Tyr	Gly	Gly	Asp	Val	Trp	Phe	Pro	Gln	
		275					280					285				
Pro	Ala	Pro	Lys	Asp	His	Pro	Trp	Arg	Asp	Met	Arg	Asn	Lys	Tyr	Gly	
	290					295					300					
Ala	Gly	Asn	Ala	Met	Thr	Pro	His	Tyr	Ser	Gly	Thr	Thr	Leu	Asp	Ala	
305					310					315					320	
Gln	Thr	Arg	Tyr	Ala	Glu	Gly	Thr	Lys	Asn	Ile	Leu	Glu	Ser	Phe	Phe	
				325					330					335		
Thr	Gly	Lys	Phe	Asp	Tyr	Arg	Pro	Gln	Asp	Ile	Ile	Leu	Leu	Asn	Gly	
			340					345					350			
Glu	Tyr	Val	Thr	Lys	Ala	Tyr	Gly	Lys	His	Asp	Lys	Lys				
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<210> 61
<211> 1488
<212> DNA
<213> Pseudomonas putida
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<400>	61						
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tgtgaaatcc	tcgacggcag	cggccagtac	ctgatgccc	gcggcatcga	cccgcatacc		180
cacatgcagt	tgccattcat	gggcaccgtg	gccagcagagg	atttcttcag	cggcaccgca		240
gcgggccttg	ccggcggcac	cacgtcgatc	atcgacttcg	tcatcccca	cccgcagcag		300
tcattgctg	aggccttcca	cacctggcgc	ggctgggcgc	agaagagcgc	cagcgactac		360
ggcttccacg	ttgccatcac	ctggtggagc	gaacaggtag	ctgaagaaat	gggcgaactg		420
gtagccaagc	atggggtgaa	cagcttcaag	cacttcatgg	cttacaagaa	tgcaatcatg		480
gccgcccagc	acacccttgt	ggccagcttc	gagcgcctgc	tgcaactggg	tgccgtgccc		540
accgtgcatg	ccgagaacgg	cgaactggtg	taccacctgc	agaaaaaac	gcttgcccag		600
ggcatgaccg	gaccagaggc	tcacccctt	tcgcgccctt	cacaagtgga	aggtgaagcg		660
gccagccgcg	ccatccgtat	tgccgaaacc	attggtacgc	cgctgtatgt	ggtgcacatt		720
tccagccgtg	aagcactgga	tgaaatcacc	tatgcacgcg	ccaagggcca	gccggtttac		780
ggcgaagtct	tgcccggcca	cctgctgctg	gacgacagcg	tctaccgtga	cccggactgg		840
gccactgccg	ctggctacgt	gatgagccc	ccgttccgcc	cgcgcaqca	ccaggaggcg		900

ctgtggcgcg	gcttgcagtc	gggcaacctg	cacaccacgg	ccaccgacca	ctgctgtttc	960
tgcgccgaac	agaaagccat	gggccgcgac	gacttcagtc	gcatcccca	cggcaccgcc	1020
ggcatcgaag	accgcatggc	ggtgctgtgg	gatgccggtg	tcaacagcgg	gcgcctgtcg	1080
atgcatgagt	tcgttgcgct	gacctccacc	aacacggcaa	aaatcttcaa	ccttttccca	1140
cgcaagggcg	ccatccgcgt	gggtgccgac	gccgacctgg	tgctgtggga	cccgcagggc	1200
actcgcactc	tatcgggcca	gacccaccac	cagcgggtgg	acttcaatat	ctttgaaggc	1260
cgcactgtgc	gcgggggtccc	cagccacacc	atcagccagg	gcaagggtgct	ctggggccgat	1320
ggcgacctgc	gtcgccgagg	ccggggcggg	gcggtatgtg	gaacggcccg	cgtatccgtc	1380
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<210> 62
<211> 495
<212> PRT
<213> Pseudomonas putida
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<400> 62

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20 25 30

Pro Asn Leu Glu Pro Pro Thr Asp Cys Glu Ile Leu Asp Gly Ser Gly
35 40 45

Gln Tyr Leu Met Pro Gly Gly Ile Asp Pro His Thr His Met Gln Leu
50 55 60

Pro Phe Met Gly Thr Val Ala Ser Glu Asp Phe Phe Ser Gly Thr Ala
65 70 75 80

Ala Gly Leu Ala Gly Gly Thr Thr Ser Ile Ile Asp Phe Val Ile Pro
85 90 95

Asn Pro Gln Gln Ser Leu Leu Glu Ala Phe His Thr Trp Arg Gly Trp
100 105 110

Ala Gln Lys Ser Ala Ser Asp Tyr Gly Phe His Val Ala Ile Thr Trp
115 120 125

Trp Ser Glu Gln Val Ala Glu Glu Met Gly Glu Leu Val Ala Lys His
130 135 140

Gly Val Asn Ser Phe Lys His Phe Met Ala Tyr Lys Asn Ala Ile Met
145 150 155 160

Ala Ala Asp Asp Thr Leu Val Ala Ser Phe Glu Arg Cys Leu Gln Leu
165 170 175

Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	His
180			185			190									
Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	His
195			200			205									
Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	Ala
210			215			220									
Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	Ile
225			230			235									
Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	Gly
245			250			255									
Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	Asp
260			265			270									
Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	Met
275			280			285									
Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	Gly
290			295			300									
Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	Phe
305			310			315									
Cys	Ala	Glu	Gln	Lys	Ala	Met	Gly	Arg	Asp	Asp	Phe	Ser	Arg	Ile	Pro
325			330			335									
Asn	Gly	Thr	Ala	Gly	Ile	Glu	Asp	Arg	Met	Ala	Val	Leu	Trp	Asp	Ala
340			345			350									
Gly	Val	Asn	Ser	Gly	Arg	Leu	Ser	Met	His	Glu	Phe	Val	Ala	Leu	Thr
355			360			365									
Ser	Thr	Asn	Thr	Ala	Lys	Ile	Phe	Asn	Leu	Phe	Pro	Arg	Lys	Gly	Ala
370			375			380									
Ile	Arg	Val	Gly	Ala	Asp	Ala	Asp	Leu	Val	Leu	Trp	Asp	Pro	Gln	Gly
385			390			395									
Thr	Arg	Thr	Leu	Ser	Ala	Gln	Thr	His	His	Gln	Arg	Val	Asp	Phe	Asn
405			410			415									
Ile	Phe	Glu	Gly	Arg	Thr	Val	Arg	Gly	Val	Pro	Ser	His	Thr	Ile	Ser
420			425			430									
Gln	Gly	Lys	Val	Leu	Trp	Ala	Asp	Gly	Asp	Leu	Arg	Arg	Arg	Gly	Arg
435			440			445									
Gly	Gly	Ala	Val	Cys	Gly	Thr	Ala	Gly	Val	Ser	Val	Gly	Val	Arg	Gly
450			455			460									
Ala	Gly	Ala	Thr	Arg	Arg	Thr	Ala	Ala	Pro	Asp	Ala	Arg	Ser	Ala	Leu
465			470			475									
Arg	Pro	Leu	Gly	Leu	Leu	Arg	Ser	Pro	Ser	Pro	Ala	Ser	Gln	Ile	
485			490			495									

00000000 - 00000000

44

305				310				315				320			
Phe	Cys	Ala	Glu	Gln 325	Lys	Ala	Met	Gly	Arg 330	Asp	Asp	Phe	Ser	Arg 335	Ile
Pro	Asn	Gly	Thr 340	Ala	Gly	Ile	Glu	Asp 345	Arg	Met	Ala	Val	Leu 350	Trp	Asp
Ala	Gly	Val 355	Asn	Ser	Gly	Arg	Leu 360	Ser	Met	His	Glu	Phe 365	Val	Ala	Leu
Thr	Ser 370	Thr	Asn	Thr	Ala	Lys 375	Ile	Phe	Asn	Leu	Phe 380	Pro	Arg	Lys	Gly
Ala 385	Ile	Arg	Val	Gly	Ala 390	Asp	Ala	Asp	Leu	Val 395	Leu	Trp	Asp	Pro	Gln 400
Gly	Thr	Arg	Thr	Leu 405	Ser	Ala	Gln	Thr	His 410	His	Gln	Arg	Val	Asp 415	Phe
Asn	Ile	Phe 420	Glu	Gly	Arg	Thr	Val	Arg 425	Gly	Val	Pro	Ser	His 430	Thr	Ile
Ser	Gln	Gly 435	Lys	Val	Leu	Trp	Ala 440	Asp	Gly	Asp	Leu	Arg 445	Arg	Arg	Gly
Arg	Gly 450	Gly	Ala	Val	Cys	Gly 455	Thr	Ala	Gly	Val	Ser 460	Val	Gly	Val	Arg
Gly 465	Ala	Gly	Ala	Thr 470	Arg	Arg	Thr	Ala	Ala	Pro 475	Asp	Ala	Arg	Ser	Ala 480
Leu	Arg	Pro	Leu	Gly 485	Leu	Leu	Arg	Ser	Pro 490	Ser	Pro	Ala	Ser	Gln 495	Ile

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<210> 65
<211> 1683
<212> DNA
<213> Penicillium simplicissimum
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catcatgtca	tggaccagga	ctacttcctt	gcctcagcaa	ttgttgctcc	tcgcaatgtc		240
gccgatgtgc	agtcgattgt	cggacttgcc	aataagttct	catttcccct	ctggcccatc		300
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ctggacatgg	gaaagaatat	gaacagagtt	ctagaagtga	acgtggaagg	cgcatattgc		420
gtggtggagc	ccggtgtaac	ttaccacgac	ttgcataatt	accttgaggc	gaacaatctt		480
cgagacaaat	tatggcttga	tgtaccggat	cttggtggcg	gttctgttct	cggcaatgcc		540
gttgagagag	gtgtgggcta	tacgccttac	ggagatcatt	ggatgatgca	cagtgggatg		600

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aaacgtcccg aaacgatggg gctaaagcca gaagaccagc catggagcaa aatcgctcat 720
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attgttacca agatcgggat ctggttaatg cccaatccag ggggttatca atcctacttg 840
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aacagcagct tcctaagggt caatgagggt ctcaagaatg cggtggatcc taatggcatc 1620
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taa 1683

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<210> 66
<211> 560
<212> PRT
<213> Penicillium simplicissimum

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<400> 66

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20          25          30
Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val Asp
35          40          45
Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val Met
50          55          60
Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn Val
65          70          75          80

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003021" 2E24E460

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Leu	Trp	Pro	Ile	Ser	Ile	Gly	Arg	Asn	Ser	Gly	Tyr	Gly	Gly	Ala	Ala
			100					105					110		
Pro	Arg	Val	Ser	Gly	Ser	Val	Val	Leu	Asp	Met	Gly	Lys	Asn	Met	Asn
		115					120					125			
Arg	Val	Leu	Glu	Val	Asn	Val	Glu	Gly	Ala	Tyr	Cys	Val	Val	Glu	Pro
	130					135					140				
Gly	Val	Thr	Tyr	His	Asp	Leu	His	Asn	Tyr	Leu	Glu	Ala	Asn	Asn	Leu
145					150					155					160
Arg	Asp	Lys	Leu	Trp	Leu	Asp	Val	Pro	Asp	Leu	Gly	Gly	Gly	Ser	Val
				165					170					175	
Leu	Gly	Asn	Ala	Val	Glu	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	Asp
			180					185					190		
His	Trp	Met	Met	His	Ser	Gly	Met	Glu	Val	Val	Leu	Ala	Asn	Gly	Glu
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	210					215					220				
Thr	Met	Gly	Leu	Lys	Pro	Glu	Asp	Gln	Pro	Trp	Ser	Lys	Ile	Ala	His
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Ser	Asn	Met	Gly	Ile	Val	Thr	Lys	Ile	Gly	Ile	Trp	Leu	Met	Pro	Asn
			260					265					270		
Pro	Gly	Gly	Tyr	Gln	Ser	Tyr	Leu	Ile	Thr	Leu	Pro	Lys	Asp	Gly	Asp
		275					280					285			
Leu	Lys	Gln	Ala	Val	Asp	Ile	Ile	Arg	Pro	Leu	Arg	Leu	Gly	Met	Ala
	290					295					300				
Leu	Gln	Asn	Val	Pro	Thr	Ile	Arg	His	Ile	Leu	Leu	Asp	Ala	Ala	Val
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Leu	Gly	Asp	Lys	Arg	Ser	Tyr	Ser	Ser	Lys	Thr	Glu	Pro	Leu	Ser	Asp
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Glu	Glu	Leu	Asp	Lys	Ile	Ala	Lys	Gln	Leu	Asn	Leu	Gly	Arg	Trp	Asn
			340					345					350		
Phe	Tyr	Gly	Ala	Leu	Tyr	Gly	Pro	Glu	Pro	Ile	Arg	Arg	Val	Leu	Trp
		355					360					365			
Glu	Thr	Ile	Lys	Asp	Ala	Phe	Ser	Ala	Ile	Pro	Gly	Val	Lys	Phe	Tyr
	370					375					380				
Phe	Pro	Glu	Asp	Thr	Pro	Glu	Asn	Ser	Val	Leu	Arg	Val	Arg	Asp	Lys
385					390					395					400
Thr	Met	Gln	Gly	Ile	Pro	Thr	Tyr	Asp	Glu	Leu	Lys	Trp	Ile	Asp	Trp

415

Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu
545 550 555 560

<213> Artificial Sequence

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Ala	Pro	Arg	Val	Ser	Gly	Ser	Val	Val	Leu	Asp	Met	Gly	Lys	Asn	Met
		115					120					125			
Asn	Arg	Val	Leu	Glu	Val	Asn	Val	Glu	Gly	Ala	Tyr	Cys	Val	Val	Glu
	130					135					140				
Pro	Gly	Val	Thr	Tyr	His	Asp	Leu	His	Asn	Tyr	Leu	Glu	Ala	Asn	Asn
145					150					155					160
Leu	Arg	Asp	Lys	Leu	Trp	Leu	Asp	Val	Pro	Asp	Leu	Gly	Gly	Gly	Ser
				165					170					175	
Val	Leu	Gly	Asn	Ala	Val	Glu	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly
			180					185					190		
Asp	His	Trp	Met	Met	His	Ser	Gly	Met	Glu	Val	Val	Leu	Ala	Asn	Gly
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Glu	Leu	Leu	Arg	Thr	Gly	Met	Gly	Ala	Leu	Pro	Asp	Pro	Lys	Arg	Pro
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His	Leu	Phe	Pro	Tyr	Gly	Phe	Gly	Pro	Tyr	Ile	Asp	Gly	Leu	Phe	Ser
				245					250					255	
Gln	Ser	Asn	Met	Gly	Ile	Val	Thr	Lys	Ile	Gly	Ile	Trp	Leu	Met	Pro
			260					265					270		
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		275					280					285			
Asp	Leu	Lys	Gln	Ala	Val	Asp	Ile	Ile	Arg	Pro	Leu	Arg	Leu	Gly	Met
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Ala	Leu	Gln	Asn	Val	Pro	Thr	Ile	Arg	His	Ile	Leu	Leu	Asp	Ala	Ala
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Val	Leu	Gly	Asp	Lys	Arg	Ser	Tyr	Ser	Ser	Lys	Thr	Glu	Pro	Leu	Ser
				325					330					335	
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Asn	Phe	Tyr	Gly	Ala	Leu	Tyr	Gly	Pro	Glu	Pro	Ile	Arg	Arg	Val	Leu
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Trp	Glu	Thr	Ile	Lys	Asp	Ala	Phe	Ser	Ala	Ile	Pro	Gly	Val	Lys	Phe
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Tyr	Phe	Pro	Glu	Asp	Thr	Pro	Glu	Asn	Ser	Val	Leu	Arg	Val	Arg	Asp
385					390					395					400
Lys	Thr	Met	Gln	Gly	Ile	Pro	Thr	Tyr	Asp	Glu	Leu	Lys	Trp	Ile	Asp
				405					410					415	
Trp	Leu	Pro	Asn	Gly	Ala	His	Leu	Phe	Phe	Ser	Pro	Ile	Ala	Lys	Val
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445

Leu

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<210> 70
 <211> 283
 <212> PRT
 <213> Candida magnoliae

<400> 70

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His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
			20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala	
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Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
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Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
65					70					75					80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
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Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
			100					105					110			
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
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Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
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				165					170					175		
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Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
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Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp	
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Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
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Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
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280

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THE CHINESE

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<210> 73
 <211> 533
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 73

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			20					25					30		
Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	Thr
			35					40					45		
Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	Glu
			50					55				60			
Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	Thr
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<211> 1605
<212> DNA
<213> Artificial Sequence
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Q&A with the President

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<210> 75
<211> 534
<212> PRT
<213> Artificial Sequence

<400> 75

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Tyr	Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	35	40	45	
Thr	Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	50	55	60	
Glu	Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	65	70	75	80
Thr	Leu	Val	Ala	Ser	Val	Leu	Ala	Asn	Lys	His	Asn	Val	Glu	Phe	Gln	85	90	95	
Thr	Lys	Glu	Gly	Val	Lys	Gln	Pro	Asn	Tyr	Phe	Gly	Ser	Met	Thr	Gln	100	105	110	
Cys	Ser	Thr	Leu	Lys	Leu	Gly	Ile	Asp	Ala	Glu	Gly	Asn	Asp	Val	Tyr	115	120	125	
Ala	Pro	Phe	Asn	Ser	Leu	Leu	Pro	Met	Val	Ser	Pro	Asn	Asp	Phe	Val	130	135	140	
Val	Ser	Gly	Trp	Asp	Ile	Asn	Asn	Ala	Asp	Leu	Tyr	Glu	Ala	Met	Gln				

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<210> 77
 <211> 680
 <212> PRT
 <213> Hypomyces rosellus
 <400> 77

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 Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
 50 55 60
 Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
 65 70 75 80
 His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
 85 90 95
 Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
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 Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
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 Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser Gly

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Ser Trp Phe Ala Asp	Ser Thr Thr Lys Tyr	Ser Asn Phe Glu Thr Arg		
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Pro Ala Arg Tyr Val	Arg Leu Val Ala Ile	Thr Glu Ala Asn Gly Gln		
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Pro Trp Thr Ser Ile	Ala Glu Ile Asn Val	Phe Gln Ala Ser Ser Tyr		
	180	185		190
Thr Ala Pro Gln Pro	Gly Leu Gly Arg Trp	Gly Pro Thr Ile Asp Leu		
	195	200		205
Pro Ile Val Pro Ala	Ala Ala Ala Ile Glu	Pro Thr Ser Gly Arg Val		
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Leu Met Trp Ser Ser	Tyr Arg Asn Asp Ala	Phe Gly Gly Ser Pro Gly		
	225	230		235
Gly Ile Thr Leu Thr	Ser Ser Trp Asp Pro	Ser Thr Gly Ile Val Ser		
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Ser Met Asp Gly Asn	Gly Gln Ile Val Val	Thr Gly Gly Asn Asp Ala		
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Lys Lys Thr Ser Leu	Tyr Asp Ser Ser Ser	Asp Ser Trp Ile Pro Gly		
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Pro Asp Met Gln Val	Ala Arg Gly Tyr Gln	Ser Ser Ala Thr Met Ser		
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	370	375		380
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Gly Val Ala Pro Asp	Ala Met Cys Gly Asn	Ala Val Met Tyr Asp Ala		
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Val Lys Gly Lys Ile	Leu Thr Phe Gly Gly	Ser Pro Asp Tyr Gln Asp		
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Ser Asp Ala Thr Thr	Asn Ala His Ile Ile	Thr Leu Gly Glu Pro Gly		
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